

Table 1-1

GENE NAME/SEQ ID NO*	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
atrial regulatory myosin	7	5	3	13	2	2	10	5	1	7	5	9	7	3	1	2
ventricular myosin alkali light chain	5	4	4	18	8	9	9	4	2	11	6	6	14	8	5	4
troponin	6	5	5	10	3	1	10	5	1	8	7	8	6	2	1	0
cardiac ventricular myosin	4	4	3	19	6	9	7	4	2	8	7	5	17	5	7	5
cardiodilatin	4	3	4	10	2	1	5	3	1	4	5	7	4	1	1	0
creatine kinase M	6	4	6	16	9	9	7	4	2	10	8	6	21	6	8	5
myoglobin	4	4	6	17	8	10	7	4	2	9	5	8	19	3	9	3
natriuretic peptide precursor	6	6	2	9	0	1	5	6	1	5	2	6	4	1	2	1
sarcomeric mitoch. creatine kinase	7	4	7	16	7	5	8	4	2	11	6	6	12	3	5	2
telethonin	4	4	7	15	6	8	8	4	2	12	6	5	18	6	7	6
titin	4	4	6	18	9	11	5	4	2	11	8	5	22	5	10	7
urocortin	2	1	1	7	2	5	3	1	6	5	2	2	5	2	6	6

\* entries in the table are the negative log of the p-value; an entry of 5 or greater is highly significant.

Table 1-2

GENE NAME	SEQ ID NO*	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
atrial regulatory myosin		2	2	4	10	7	8	1	6	6	11	15	7	2	12	1	2
ventricular myosin alkali light chain		6	1	10	8	10	6	5	7	9	15	19	17	2	11	5	4
tropoin		2	0	4	5	5	10	0	6	5	9	14	7	3	9	0	0
cardiac ventricular myosin		7	2	9	9	8	5	6	5	7	14	16	18	4	10	6	7
cardiodilatin		1	0	2	7	5	5	1	4	3	6	8	5	1	9	0	1
creatine kinase M		7	0	11	9	7	7	7	7	7	18	17	21	4	14	4	8
myoglobin		7	2	9	13	8	7	10	5	7	14	16	20	3	15	6	6
natriuretic peptide precursor		3	1	4	5	9	3	1	2	5	6	12	5	1	10	1	2
sarcomeric mitoch. creatine kinase		6	0	10	9	7	8	5	5	6	14	13	15	5	13	5	6
telethonin		8	1	9	9	7	8	9	3	8	14	16	19	1	14	7	7
titin		5	2	10	12	9	7	11	6	5	16	15	18	4	14	6	7
urocortin		3	6	5	4	4	3	4	1	3	6	6	3	2	8	6	4

\* entries in the table are the negative log of the p-value; an entry of 5 or greater is highly significant.

Table 1-3

GENE NAME/SEQ ID NO*	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
atrial regulatory myosin	8	9	1	5	10	11	9	3	11	4	3	2	5	7	9	3
ventricular myosin alkali light chain	7	7	6	5	14	8	13	11	18	5	4	3	8	10	9	9
troponin	6	8	3	4	10	10	10	4	10	4	5	3	3	8	5	2
cardiac ventricular myosin	6	7	8	7	14	7	16	10	15	6	6	4	6	11	8	7
cardiodilatin	4	4	2	1	6	10	5	2	8	6	5	7	3	5	2	2
creatine kinase M	8	7	8	4	13	8	21	11	20	7	3	4	7	11	7	6
myoglobin	8	7	5	4	16	11	20	9	19	6	5	6	8	9	8	7
natriuretic peptide precursor	5	4	1	1	4	6	8	2	7	2	1	2	4	5	3	4
sarcomeric mitoch. creatine kinase	9	5	7	3	13	8	19	7	17	5	4	4	7	9	8	5
telethonin	10	7	6	4	9	6	20	10	19	4	4	2	10	8	7	9
titin	11	7	8	5	11	7	17	9	19	8	3	4	9	11	8	6
urocortin	2	4	3	3	9	3	7	3	7	1	1	2	4	3	7	6

\* entries in the table are the negative log of the p-value; an entry of 5 or greater is highly significant.

Table 2

SEQ ID No:	Amino Acid Residues	Potential Phosphorylation Sites	Potential glycosylation sites	Signature Sequence	Identification	Analytical Methods
49	70	S46				Motif
50	552	S541 S11 S15 S26 S54 S99 S108 T118 S125 S134 S168 T197 T250 S312 S502 S520 T56 S77 T143 T281 S392 S400 T409 S435 S499 S511 S533	N148 N174 N177 N223 N325	K402 to T456 Synapsins	Tropomodulin synapsin	Motif, BLAST BLOCKS
51	260	S35 S51 T124 S171 S183 Y154				Motif
52	364	T103 T125 T247 T274 S329 S5 S162 S242 S282	N4	M1 to G49 Signal Peptide m42 TO c64 and D76 to C88 receptor signatures F173 to F182 Glycosyl hydrolases signature	Receptor glycosyl hydrolase	Motif, SigPept PRINTS, BLOCKS
53	527	S168 S232 S239 T314 S315 T332 T344 T373 T496 T512 S524				Motif
54	82	T63 T67	N29			Motif
56	193	S4 S6 T60 S86 S148 T157 T60 T126	N2	L86 to Y122 Phosphatase transforming 61K PDF1	HET-C, glycolipid transfer protein	Motif, BLAST BLOCKS_DOMO
57	174	T49 S40 T72 S81 S21 S57 S141	N19	L8 to L29leucine zipper pattern Y27 to E42 and E103 to L118 secretin receptor E54 to K71 and E103 to E131 tropomysin receptor Q95 to T148 tropomysin	CNN, mitotin, tropomysin	Motif, BLAST BLOCKS, PRINTS

Table 2 (cont.)

58	230	S27 T33 S58 T75 T209		S23 Glycosaminoglycan attachement site P84 TO P95 Aminoacyl tRNA synthetase class-1 signature V119 to H129 glycosyl transferase signature	Glycosyl Transferase	Motif, BLOCKS
59	915	T775 T56 S58 S74 T100 S140 S224 T240 S241 S291 T292 S308 S314 T320 S353 S367 T375 S382 S414 T422 S428 S455 T480 T502 S503 S513 S529 T608 T674 S767 T796 T20 T179 S329 T343 T361 T369 S406 S538 S641 T668 S740 T849 S911 Y119 Y360	N426 N633	L530 to S641 and P650 to S734 fn family, L607 to Y625 and Y718 to E732 fibronectin V627 to G636 and F720 to G729 receptor glycoprotein signature	Ring finger protein, zincfinger protein RFP fibronectin	Motif, BLAST PRINTS, BLOCKS, Pfam
60	163	S125 S94		F74 to A93 smooth muscle protein 22 G83 to S94 proteoglycan C- terminal	Smooth muscle protein, proteoglycan	Motif, BLOCKS_DOMO PRINTS
62	329	S68 T67 T284 S318	N316	R28 "RGD" cell attachment sequence L154 to L169, M187 to L202, L220 to F235, G249 to R258, and L253 to L268 ankyrin repeats	Cardiac ankyrin repeat protein	Motif, BLAST, PRINTS, BLOCKS, Pfam